Amendments to the Specification:

Please replace paragraph **[0019]** beginning at page 6, line 25, with the following:

--**[0019]** In another set of embodiments, the invention provides methods for lysing erythrocytes adherent due to a pathological condition, said method comprising administering to a patient with said pathologically adherent erythrocytes a nucleic acid encoding a peptide with at least 80% sequence identity to the sequence $YX_1TFSX_2LIX_3IFQX_4X_5$ (SEQ ID NO:6), or fragment thereof which raises antibodies which specifically recognize said peptide, wherein X_1, X_2, X_3, X_4 and X_5 are independently selected from amino acids that bear a charge at physiological pH, wherein expression of said peptide raises antibodies which specifically bind to and cause lysis of said pathologically adherent erythrocytes. In some embodiments, X_1 and X_4 bear the same charge and X_2 and X_3 bear the same charge, but the charge borne by X_1 and X_4 is not the same as the charge borne by X_2 and X_3. In some of the methods, the charge borne by X_2 and X_3 is positive and in some, X_2 and X_3 are lysine residues. In some embodiments, the peptide has 100% sequence identity to ~~SEQ ID:6~~ SEQ ID NO:6 and further X_2 and X_3 are lysine residues, X_1 is a glutamic acid, X_4 is an aspartic acid and X_5 is a histidine (SEQ ID NO:5).--

Please replace paragraph **[0030]** beginning at page 9, line 21, with the following:

--**[0030] Figure 7.** Predicted secondary structure of the DBR peptide. The central 10 amino acid core assumes a highly alpha-helical structure. The top line is a bar graph indicating the confidence of prediction. The next line down is a cartoon showing the position of the predicted helix. The third line down indicates with an "H" if the amino acid at the indicated position in the DBR peptide is predicted to be in an alpha-helix, or "C", if the amino acid at the indicated position is predicted not to be in an alpha-helix. The following line sets out the sequence of the DBR peptide (SEQ ID NO:5).--

Please replace paragraph **[0035]** beginning at page 11, line 3, with the following:

--**[0035]** The present studies indicate that residues 536 to 545 of the AE1 protein (TFSKLIKIFQ, ~~SEQ ID NO:5~~ SEQ ID NO:3), form an alpha-helix, as shown in Figure 7. Without wishing to be bound by theory, it appears that antibodies directed to the alpha helix formed by the amino acids of ~~SEQ ID NO:5~~ SEQ ID NO:3, and perhaps especially to epitopes that include the amino terminal end of ~~SEQ ID NO:5~~ SEQ ID NO:3, are particularly useful in marking for lysis cells with exposure of this normally cryptic portion of AE1.--

Please replace paragraph **[0041]** beginning at page 12, line 30, with the following:

--**[0041]** Fragments of the peptides, particularly fragments containing the amino terminal portion of the peptide of SEQ ID NOS:5 or 6, can also be used. For example, YETFSKLIK ~~(SEQ ID NO:21)~~ (SEQ ID NO:22) or YDTFSRLIR ~~(SEQ ID NO:22)~~ (SEQ ID NO:23) may also be used. As noted, any particular peptide can be tested to confirm whether it generates antibodies that bind to and cause lysis of cells with exposed normally cryptic portions of AE1 by assays known in the art, such as those taught in the Examples.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 10, at the end of the application.